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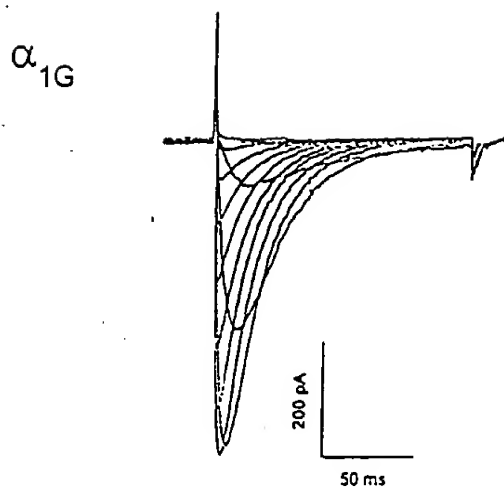


Fig. 1A

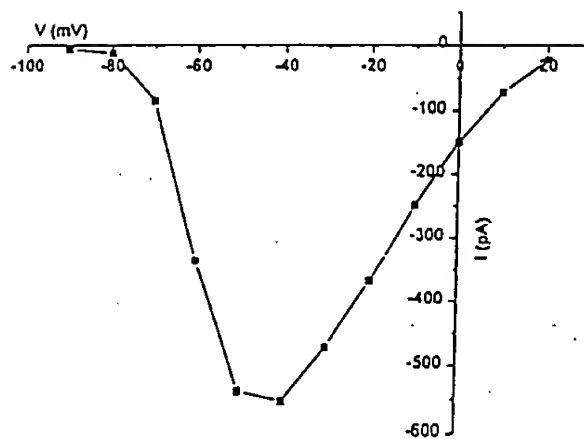


Fig. 1B

$\alpha_{11}$

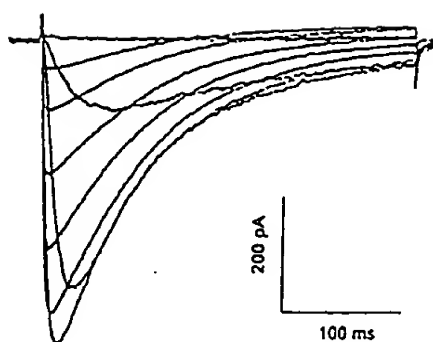


Fig. 2A

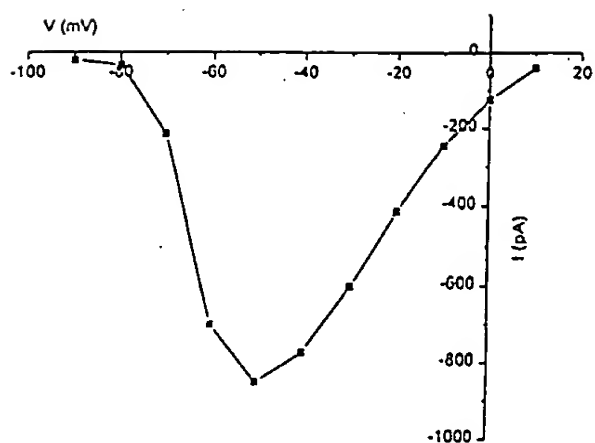


Fig. 2 B

# Steady-state inactivation

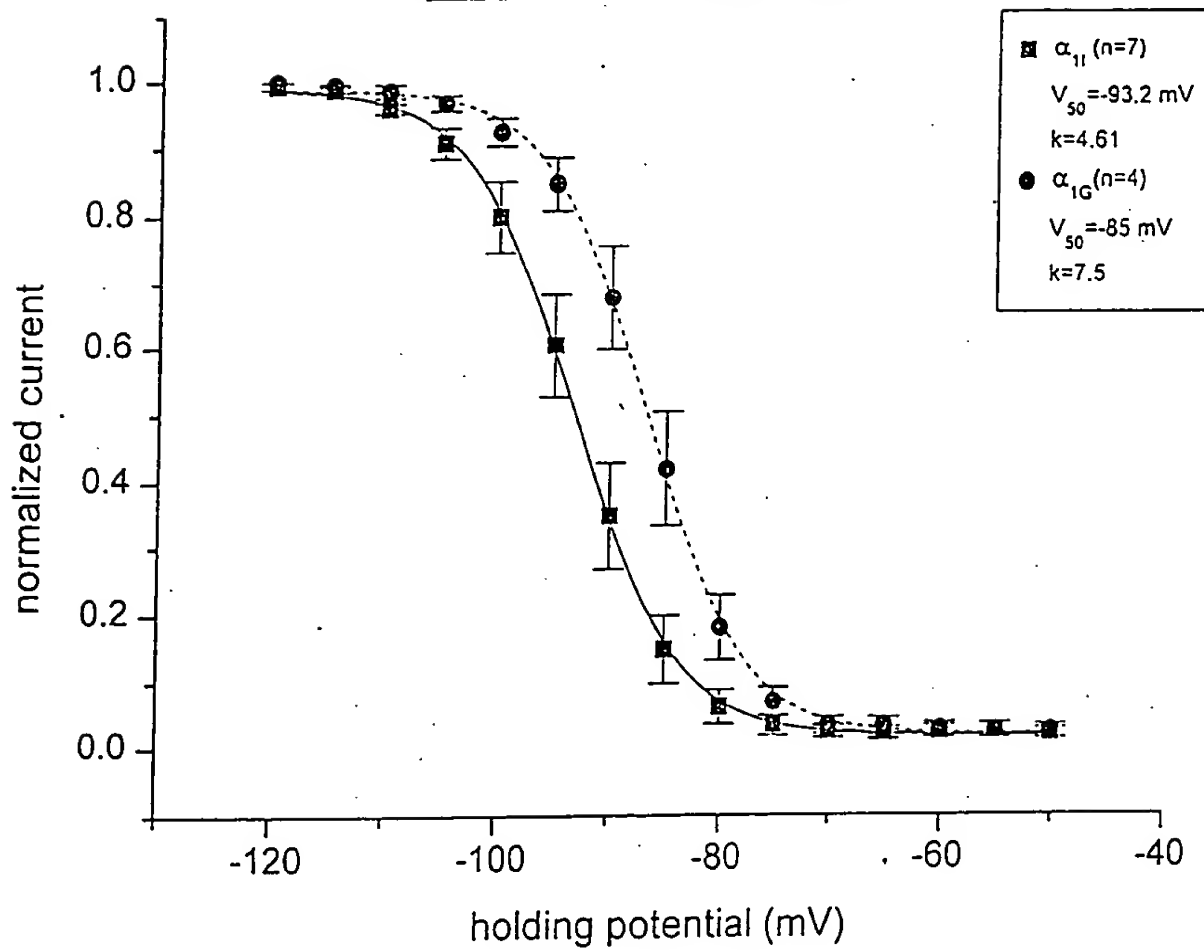
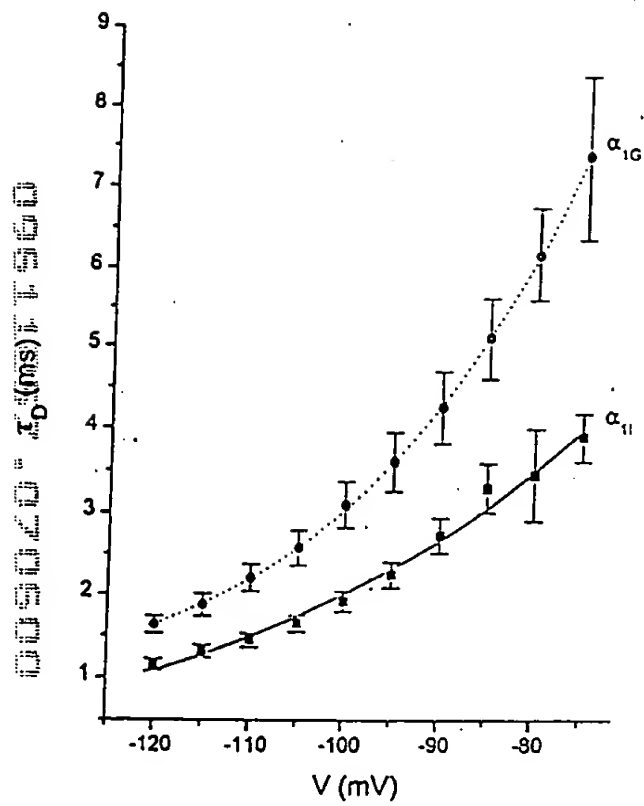


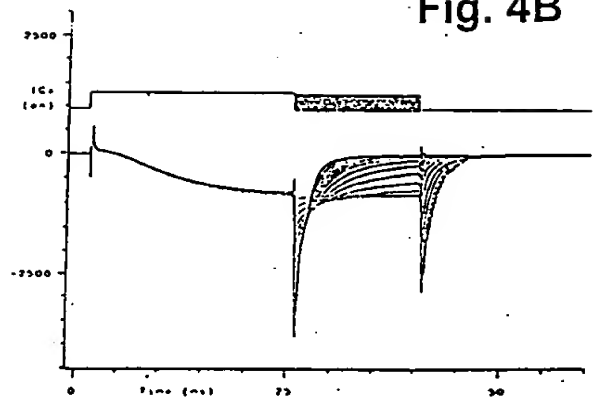
Fig. 3

Deactivation



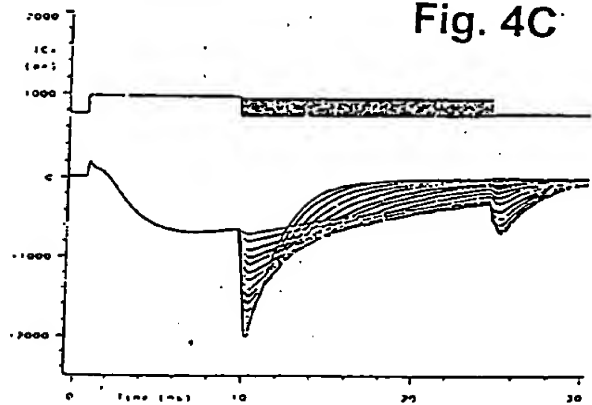
$\alpha_{1I}$

Fig. 4B



$\alpha_{1G}$

Fig. 4C



5

Figure A.  $\alpha$ 1G cDNA construct

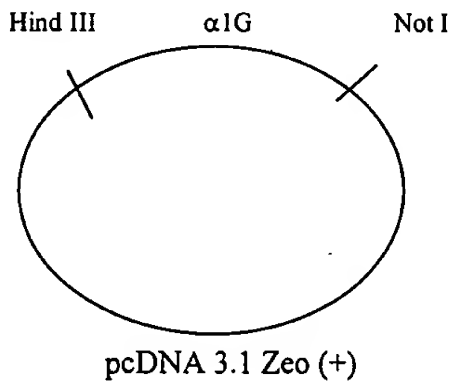
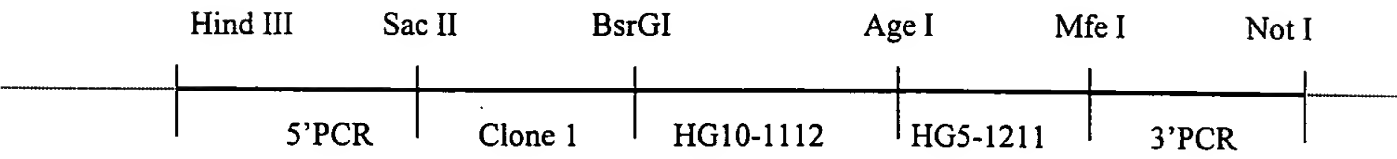
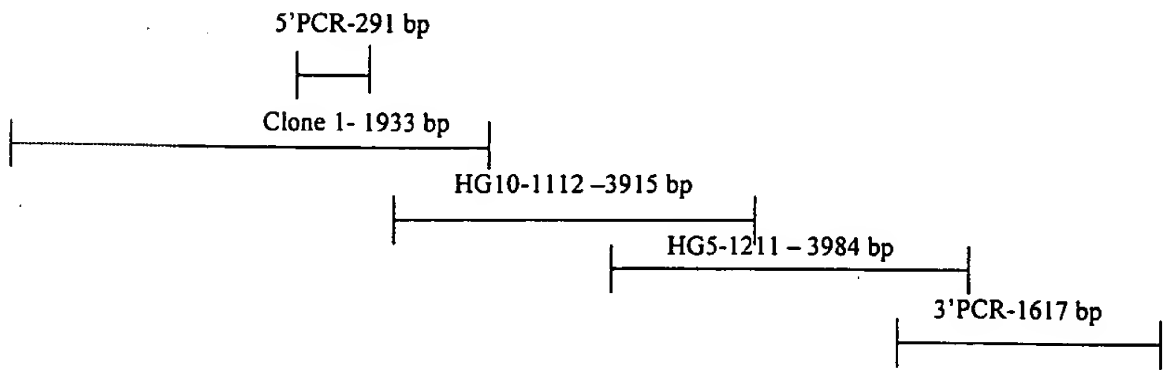


Figure B.  $\alpha$ 1G cDNA CLONES



# Human $\alpha 1$ G T-type calcium channel cDNA

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1 M D E E E D G 7
72 GCG GGC GCC GAG GAG TCG GGA CAG CCC CGG AGC TTC ATG CGG CTC AAC GAC CTG TCG GGG 131
8 A G A E E S G Q P R S F M R L N D L S G 27
132 GCC GGG GGC CGG CCG GGG CCG GGG TCA GCA GAA AAG GAC CCG GGC AGC GCG GAC TCC GAG 191
28 A G G R P G P G S A E K D P G S A D S E 47
192 GCG GAG GGG CTG CCG TAC CCG GCG CTG GCC CCG GTG GTT TTC TTC TAC TTG AGC CAG GAC 251
48 A E G L P Y P A L A P V V F F Y L S Q D 67
252 AGC CGC CCG CGG AGC TGG TGT CTC CGC ACG GTC TGT AAC CCC TGG TTT GAG CGC ATC AGC 311
68 S R P R S W C L R T V C N P W F E R I S 87
312 ATG TTG GTC ATC CTT CTC AAC TGC GTG ACC CTG GGC ATG TTC CGG CCA TGC GAG GAC ATC 371
88 M L V I L L N C V T L G M F R P C E D I 107
372 GCC TGT GAC TCC CAG CGC TGC CGG ATC CTG CAG GCC TTT GAT GAC TTC ATC TTT GCC TTC 431
108 A C D S Q R C R I L Q A F D D F I F A F 127
432 TTT GCC GTG GAG ATG GTG GTG AAG ATG GTG GCC TTG GGC ATC TTT GGG AAA AAG TGT TAC 491
128 F A V E M V V K M V A L G I F G K K C Y 147
492 CTG GGA GAC ACT TGG AAC CGG CTT GAC TTT TTC ATC GTC ATC GCA GGG ATG CTG GAG TAC 551
148 L G D T W N R L D F F I V I A G M L E Y 167
552 TCG CTG GAC CTG CAG AAC GTC AGC TTC TCA GCT GTC AGG ACA GTC CGT GTG CTG CGA CCG 611
168 S L D L Q N V S F S A V R T V R V L R P 187
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188 L R A I N R V P S M R I L V T L L L D T 207
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248 S L P L S V D L E R Y Y Q T E N E D E S 267
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288 L R G D G G G G P P C G L D Y E A Y N S 307
972 TCC AGC AAC ACC ACC TGT GTC AAC TGG AAC CAG TAC TAC ACC AAC TGC TCA GCG GGG GAG 1031
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428 E P G S C Y E E L L K Y L V Y I L R K A 447

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Figure 6

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448	A	R	R	L	A	Q	V	S	R	A	A	G	V	R	V	G	L	L	S	S	467
1452	CCA	GCA	CCC	CTC	GGG	GGC	CAG	GAG	ACC	CAG	CCC	AGC	AGC	AGC	TGC	TCT	CGC	TCC	CAC	CGC	1511
468	P	A	P	L	G	G	Q	E	T	Q	P	S	S	S	C	S	R	S	H	R	487
1512	CGC	CTA	TCC	GTC	CAC	CAC	CTG	GTG	CAC	CAC	CAC	CAC	CAC	CAT	CAC	CAC	CAC	TAC	CAC	CTG	1571
488	R	L	S	V	H	H	L	V	H	H	H	H	H	H	H	H	H	Y	H	L	507
1572	GGC	AAT	GGG	ACG	CTC	AGG	GCC	CCC	CGG	GCC	AGC	CCG	GAG	ATC	CAG	GAC	AGG	GAT	GCC	AAT	1631
508	G	N	G	T	L	R	A	P	R	A	S	P	E	I	Q	D	R	D	A	N	527
1632	GGG	TCC	CGC	AGG	CTC	ATG	CTG	CCA	CCA	CCC	TCG	ACG	CCT	GCC	CTC	TCC	GGG	GCC	CCC	CCT	1691
528	G	S	R	R	L	M	L	P	P	P	S	T	P	A	L	S	G	A	P	P	547
1692	GGT	GGC	GCA	GAG	TCT	GTG	CAC	AGC	TTC	TAC	CAT	GCC	GAC	TGC	CAC	TTA	GAG	CCA	GTC	CGC	1751
548	G	G	A	E	S	V	H	S	F	Y	H	A	D	C	H	L	E	P	V	R	567
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588	K	V	Y	P	T	V	H	T	S	P	P	P	E	T	L	K	E	K	A	L	607
1872	GTA	GAG	GTG	GCT	GCC	AGC	TCT	GGG	CCC	CCA	ACC	CTC	ACC	AGC	CTC	AAC	ATC	CCA	CCC	GGG	1931
608	V	E	V	A	A	S	S	G	P	P	T	L	T	S	L	N	I	P	P	G	627
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628	P	Y	S	S	M	H	K	L	L	E	T	Q	S	T	G	A	C	Q	S	S	647
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5472 ATC TCG CCT ATC TAC TTT GTG TCC TTC GTG CTG ACG GCC CAG TTC GTG CTA GTC AAC GTG 5531  
1808 I S P I Y F V S F V L T A Q F V L V N V 1827

5532 GTG ATC GCC GTG CTG ATG AAG CAC CTG GAG GAG AGC AAC AAG GAG GCC AAG GAG GAG GCC 5591  
1828 V I A V L M K H L E E S N K E A K E E A 1847

5592 GAG CTA GAG GCT GAG CTG GAG CTG GAG ATG AAG ACC CTC AGC CCC CAG CCC CAC TCG CCA 5651  
1848 E L E A E L E L E M K T L S P Q P H S P 1867

5652 CTG GGC AGC CCC TTC CTC TGG CCT GGG GTC GAG GGC CCC GAC AGC CCC GAC AGC CCC AAG 5711  
1868 L G S P F L W P G V E G P D S P D S P K 1887

5712 CCT GGG GCT CTG CAC CCA GCG GCC CAC GCG AGA TCA GCC TCC CAC TTT TCC CTG GAG CAC 5771  
1888 P G A L H P A A H A R S A S H F S L E H 1907

5772 CCC ACG ATG CAG CCC CAC CCC ACG GAG CTG CCA GGA CCA GAC TTA CTG ACT GTG CGG AAG 5831  
1908 P T M Q P H P T E L P G P D L L T V R K 1927

5832 TCT GGG GTC AGC CGA ACG CAC TCT CTG CCC AAT GAC AGC TAC ATG TGT CGG CAT GGG AGC 5891  
1928 S G V S R T H S L P N D S Y M C R H G S 1947

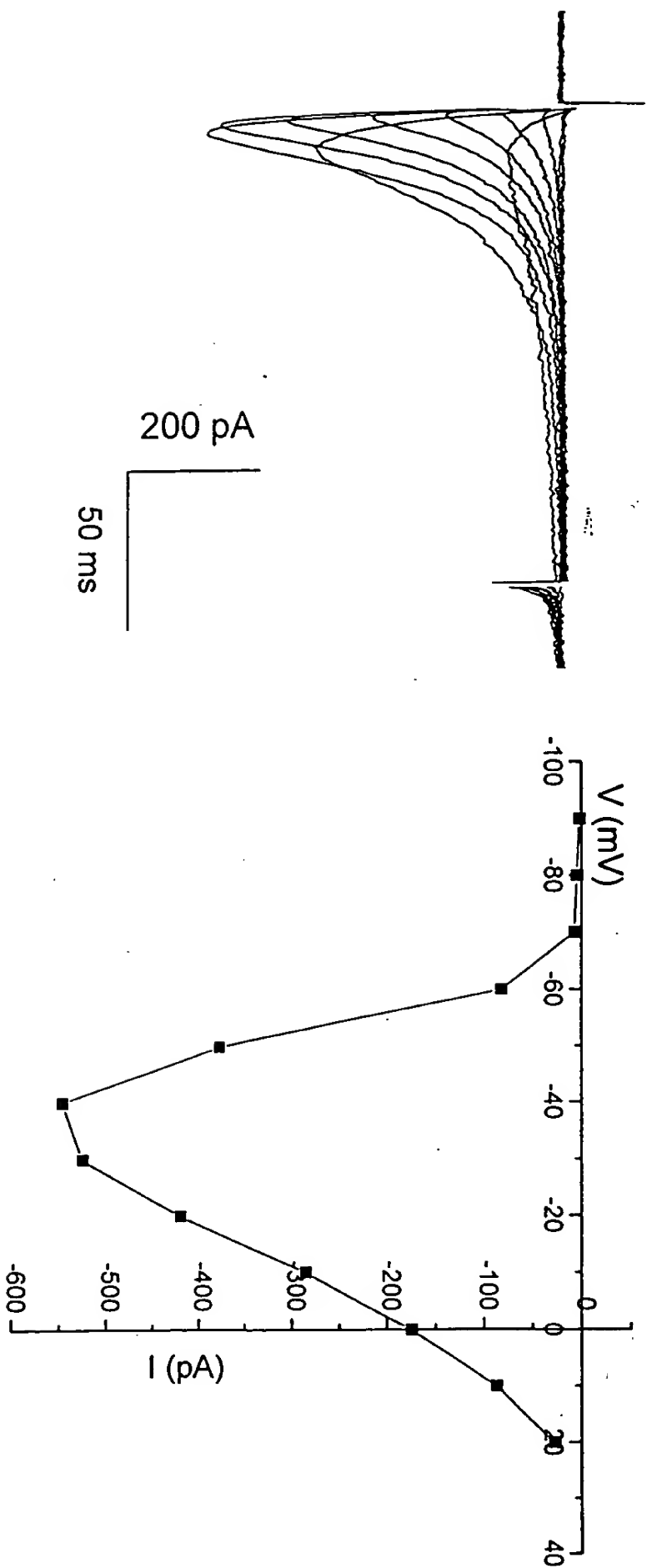
5892 ACT GCC GAG GGG CCC CTG GGA CAC AGG GGC TGG GGG CTC CCC AAA GCT CAG TCA GGC TCC 5951  
1948 T A E G P L G H R G W G L P K A Q S G S 1967

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5952	GTC	TTG	TCC	GTT	CAC	TCC	CAG	CCA	GCA	GAT	ACC	AGC	TAC	ATC	CTG	CAG	CTT	CCC	AAA	GAT	6011
1968	V	L	S	V	H	S	Q	P	A	D	T	S	Y	I	L	Q	L	P	K	D	1987
6012	GCA	CCT	CAT	CTG	CTC	CAG	CCC	CAC	AGC	GCC	CCA	ACC	TGG	GGC	ACC	ATC	CCC	AAA	CTG	CCC	6071
1988	A	P	H	L	L	Q	P	H	S	A	P	T	W	G	T	I	P	K	L	P	2007
6072	CCA	CCA	GGA	CGC	TCC	CCT	TTG	GCT	CAG	AGG	CCA	CTC	AGG	CGC	CAG	GCA	GCA	ATA	AGG	ACT	6131
2008	P	P	G	R	S	P	L	A	Q	R	P	L	R	R	Q	A	A	I	R	T	2027
6132	GAC	TCC	TTG	GAC	GTT	CAG	GGT	CTG	GGC	AGC	CGG	GAA	GAC	CTG	CTG	GCA	GAG	GTG	AGT	GGG	6191
2028	D	S	L	D	V	Q	G	L	G	S	R	E	D	L	L	A	E	V	S	G	2047
6192	CCC	TCC	CCG	CCC	CTG	GCC	CGG	GCC	TAC	TCT	TTC	TGG	GGC	CAG	TCA	AGT	ACC	CAG	GCA	CAG	6251
2048	P	S	P	P	L	A	R	A	Y	S	F	W	G	Q	S	S	T	Q	A	Q	2067
6252	CAG	CAC	TCC	CGC	AGC	CAC	AGC	AAG	ATC	TCC	AAG	CAC	ATG	ACC	CCG	CCA	GCC	CCT	TGC	CCA	6311
2068	Q	H	S	R	S	H	S	K	I	S	K	H	M	T	P	P	A	P	C	P	2087
6312	GGC	CCA	GAA	CCC	AAC	TGG	GGC	AAG	GGC	CCT	CCA	GAG	ACC	AGA	AGC	AGC	TTA	GAG	TTG	GAC	6371
2088	G	P	E	P	N	W	G	K	G	P	P	E	T	R	S	S	L	E	L	D	2107
6372	ACG	GAG	CTG	AGC	TGG	ATT	TCA	GGA	GAC	CTC	CTG	CCC	CCT	GGC	GGC	CAG	GAG	GAG	CCC	CCA	6431
2108	T	E	L	S	W	I	S	G	D	L	L	P	P	G	G	Q	E	E	P	P	2127
6432	TCC	CCA	CGG	GAC	CTG	AAG	AAG	TGC	TAC	AGC	GTG	GAG	GCC	CAG	AGC	TGC	CAG	CGC	CGG	CCT	6491
2128	S	P	R	D	L	K	K	C	Y	S	V	E	A	Q	S	C	Q	R	R	P	2147
6492	ACG	TCC	TGG	CTG	GAT	GAG	CAG	AGG	AGA	CAC	TCT	ATC	GCC	GTG	AGC	TGC	CTG	GAC	AGC	GGC	6551
2148	T	S	W	L	D	E	Q	R	R	H	S	I	A	V	S	C	L	D	S	G	2167
6552	TCC	CAA	CCC	CAC	CTG	GGC	ACA	GAC	CCC	TCT	AAC	CTT	GGG	GGC	CAG	CCT	CTT	GGG	GGG	CCT	6611
2168	S	Q	P	H	L	G	T	D	P	S	N	L	G	G	Q	P	L	G	G	P	2187
6612	GGG	AGC	CGG	CCC	AAG	AAA	AAA	CTC	AGC	CCG	CCT	AGT	ATC	ACC	ATA	GAC	CCC	CCC	GAG	AGC	6671
2188	G	S	R	P	K	K	K	L	S	P	P	S	I	T	I	D	P	P	E	S	2207
6672	CAA	GGT	CCT	CGG	ACC	CCG	CCC	AGC	CCT	GGT	ATC	TGC	CTC	CGG	AGG	AGG	GCT	CCG	TCC	AGC	6731
2208	Q	G	P	R	T	P	P	S	P	G	I	C	L	R	R	R	A	P	S	S	2227
6732	GAC	TCC	AAG	GAT	CCC	TTG	GCC	TCT	GGC	CCC	CCT	GAC	AGC	ATG	GCT	GCC	TGC	CCC	TCC	CCA	6791
2228	D	S	K	D	P	L	A	S	G	P	P	D	S	M	A	A	S	P	S	P	2247
6792	AAG	AAA	GAT	GTG	CTG	AGT	CTC	TCC	GGT	TTA	TCC	TCT	GAC	CCA	GCA	GAC	CTG	GAC	CCC	TGA	6851
2248	K	K	D	V	L	S	L	S	G	L	S	S	D	P	A	D	L	D	P	*	2267
6852	gtcctgtccccactttcccaactcacctttctccactgggtgc																				6892

006020-2541560

$\alpha_{1G}$  human 2 mM  $\text{Ca}^{2+}$



6-cyline 7  
 09611307 . 070600  
~~Figure 1~~

## COMPARISON OF P-REGIONS

I	II	III	IV	
LAASE E GWVYV	QIITQ E GWTDF	ETLSF K GWNVI	RCLTG E DWNDI	NIC-1 (C11D2.6)
LAASQ E GWVYV	QIITQ E GWTOV	ETLSY K GWNVV	RSVTG E DWNDI	NIC-2 (C27F2.3)
EASSQ E GWVFL	QILTQ E GWVDV	EVLSL K GWVEV	RIVTG E DWNKI	Rat-NIC
QCITM E GWTDV	QILTQ E DWNSV	TVSTF E GWPEL	RCATG E AWQDI	L-Type Ca Channel
QVITL E GWVDI	QILTQ E DWNKV	VLASK D GWVDI	RVSTG D NWNGI	T-Type Ca Channel
RLMTQ D FWENL	RVLCG E WIETM	QVATF K GWMDI	QITTS A GWDGL	Na Channels

Fig. 8